



227274078.ST25.txt
SEQUENCE LISTING

<110> Lang, Jas C.

<120> Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

<130> 22727/04078

B1

<140> 09/674,035

<141> 2000-12-11

<150> PCT/IB99/01818

<151> 1999-11-11

<160> 10

<170> PatentIn version 3.1

<210> 1

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Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
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ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca
Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala

96

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gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag	144
Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	
35 40 45	
acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat	192
Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	
50 55 60	
gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag	240
Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	
65 70 75 80	
aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg	288
Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	
85 90 95	
<i>B1</i> gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat	336
Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His	
100 105 110	
gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag	384
Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	
115 120 125	
gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag	432
Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys	
130 135 140	
ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa	480
Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys	
145 150 155 160	
att aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc	528
Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys	
165 170 175	
tgc gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt	576
Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val	
180 185 190	
ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg	624
Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu	
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Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr	
210 215 220	
tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc	720
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala	
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aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa	768
Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys	
245 250 255	
cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca	816
Arg Gly Leu Arg Arg Ile Val His Glu Lys Tyr Lys His Pro Ser	
260 265 270	
cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac	864

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His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr			
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Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe			
290	295	300	
caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat			960
Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn			
305	310	315	320
gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata			1008
Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile			
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gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act			1056
Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr			
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Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys			
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370	375	380	
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Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro			
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aac aag cct ggt gtt tat act aga gtt acg gcc ttg cg gac tgg att			1248
Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile			
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Thr Ser Lys Thr Gly Ile			
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35 40 45

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Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
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Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
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Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
130 135 140

B1
Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
180 185 190

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195 200 205

Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
210 215 220

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225 230 235 240

Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
245 250 255

Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
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Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
290 295 300

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Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
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Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
325 330 335

Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
340 345 350

Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
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Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
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Thr Ser Lys Thr Gly Ile
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ccc	tgg	gtt	atc	ggc	ctc	gtc	atg	ttc	ata	tcc	ctg	att	gtc	ctg	gca
Pro	Trp	Val	Ile	Gly	Leu	Val	Met	Phe	Ile	Ser	Leu	Ile	Val	Leu	Ala
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acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr 50 55 60	192
gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln 65 70 75 80	240
aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg 85 90 95	288
gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His 100 105 110	336
B1 gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag Gly Val Leu Ala His Met Leu Ile Cys Arg Phe His Ser Thr Glu 115 120 125	384
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ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu 195 200 205	624
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cat gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr 275 280 285	864

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gat ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile 325 330 335	1008
gac gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr 340 345 350	1056
cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys 355 360 365	1104
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aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile 405 410 415	1248
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35 40 45

Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
Page 7

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55

60

Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
 65 70 75 80

Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
 85 90 95

Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
 100 105 110

Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
 115 120 125

Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
 130 135 140

B1
 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
 145 150 155 160

Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
 165 170 175

Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
 180 185 190

Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 195 200 205

Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
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Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
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Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
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Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
 260 265 270

His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
 275 280 285

Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
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Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
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Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
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Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
355 360 365

Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
370 375 380

Trp Tyr Leu Ala Gly Ile Val Ser Ser Gly Asp Glu Cys Ala Lys Pro
385 390 395 400

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